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<b>(54) Title:</b> HIGH-AFFINITY TRYPTOPHAN TRANSPORTER  <b>(57) Abstract</b>  A high-affinity and extremely selective tryptophan transport system present in human monocyte-derived macrophages is disclosed. Human monocyte-derived macrophages include two distinct transporters, a high-affinity ( $k_m=290 \pm 160$ nM) transporter that is highly specific for tryptophan and a low affinity ( $k_m=27 \pm 4$ $\mu$ M) transporter that is less specific for tryptophan, consistent with the known system L. The tryptophan transport system is predominantly (86 %) sodium-independent. The high-affinity system is very specific for tryptophan and shows no transport of any other essential amino acids in the tryptophan transport concentration range. This high-affinity system is expressed at very low levels in fresh monocytes, but undergoes a 10-30 fold induction during macrophage differentiation. This high-affinity, tryptophan-selective transport system allows macrophages to take up tryptophan efficiently under conditions of very low substrate concentration, such as can occur at sites of inflammation.		

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## HIGH-AFFINITY TRYPTOPHAN TRANSPORTER

## Background of the Invention

This application claims priority to U.S.

5 Serial No. 60/067,610 entitled "Regulation of T  
Cell Activation" filed December 5, 1997; U.S.  
Serial No. 60/080,384 entitled "Regulation of  
Pregnancy" filed April 1, 1998; and U.S. Serial No.  
60/080,380 entitled "IDO Inhibitors for Use as  
10 Antiviral Agents" filed April 1, 1998, by David  
Munn and Andrew Mellor.

This invention is generally in the field of  
tryptophan transporters, and more specifically is  
drawn to a novel tryptophan transport system.

15 The United States government has rights in  
this invention by virtue of grant K08 HL3395 from  
the National Institutes of Health.

Tryptophan occupies a unique position at the  
interface between the immune system and cellular  
20 metabolism. It is the only amino acid whose level  
is specifically and selectively modified in  
response to signals of infection and inflammation.  
This is accomplished by the enzyme indoleamine 2,3-  
dioxygenase (IDO), which rapidly and selectively  
25 degrades tryptophan following induction by  
interferon- $\gamma$  (IFN $\gamma$ ) and other proinflammatory  
signals (Taylor and Feng, 1991 *FASEB J.* 5, 2516-  
2522). The IDO system, whose origins extend back  
to invertebrates (Suzuki, et al., 1996 *Biochem.*  
30 *Biophys. Acta* 1308, 41-48; Suzuki, 1994 *J. Prot.*  
*Chem.* 13, 9-13) is hypothesized to inhibit the  
replication of intracellular pathogens (Gupta, et  
al., 1994 *Infect. Immun.* 62, 2277-2284; Thomas, et  
al., 1993 *J. Immunol.* 150, 5529-5534) and to

participate in the antiproliferative effect of interferons on host cells (Aune and Pogue, 1989 *J. Clin. Invest.* 84, 863-875; Feng and Taylor 1989, *J. Clin. Invest.* 84, 863-875; Ozaki, et al., 1988, 5 *Proc. Natl. Acad. Sci. USA* 85, 1242-1246).

Tryptophan is also unique in that it is the only amino acid whose entry into the protein synthetic pathway is regulated by the immune system. Like IDO, the gene for tryptophanyl-tRNA synthetase is 10 highly induced by IFN $\gamma$  (Fleckner, et al., 1991 *Proc. Natl. Acad. Sci. USA* 88, 11520-11524; Fleckner, et al., 1991 *Proc. Natl. Acad. Sci. USA* 88, 11520-11524; Fleckner, et al., 1995 *Cytokine* 7, 70-77; Rubin, et al., 1991 *J. Biol. Chem.* 266, 24245-15 24248), which has been proposed to assist cells in competing for scarce supplies of tryptophan (Kisselev, 1993 *Biochimie* 75, 1027-103). These observations indicate that tryptophan metabolism plays an important role in host defense.

20        Activated macrophages display a marked induction of the tryptophan catabolic pathway (Werner, et al., 1987 *Life Sci.* 41, 273-280; Carlin, et al., 1989, *J. Leuk. Biol.* 45, 29-34). These cells are capable of reducing the tryptophan 25 concentration in their local microenvironment to such a low level that cellular proliferation becomes impossible. This mechanism underlies the ability of certain types of macrophages (Munn, et al., 1996 *J. Immunol.* 156, 523-532) to inhibit T 30 cell activation. In order to achieve this effect, however, macrophages must reduce the tryptophan concentration to the low nanomolar range (less than 50 nM), three orders of magnitude below its normal

level. Macrophages can continue to take up  
tryptophan efficiently at very low substrate  
concentrations, even when tryptophan is competing  
with multiple other amino acids, present at much  
5 higher concentrations, for transport into the cell.

Based on this analysis, it is postulated that  
there must be a specific, high affinity tryptophan  
transporter.

It is therefore an object of the present  
10 invention to provide a high-affinity amino acid  
transport system that is highly specific for  
tryptophan.

It is another object of the present  
description to provide methods and reagents for use  
15 in isolating and characterizing the cDNA and amino  
acid sequence of high affinity tryptophan  
transporters.

It is yet a still further object of the  
present invention to provide methods and reagents  
20 for designing and isolating molecules and drugs  
that can stimulate or inhibit the binding or  
transport of tryptophan with high affinity  
tryptophan transporters.

## 25 **Summary of the Disclosure**

A high affinity and extremely selective  
tryptophan transport system present in human  
monocyte-derived macrophages is disclosed. Human  
monocyte-derived macrophages include two distinct  
30 transporters, a high affinity ( $K_m=290 \pm 160$  nM)  
transporter that is highly specific for tryptophan  
and a low affinity ( $K_m=27 \pm 4$   $\mu$ M) transporter that  
is less specific for tryptophan, consistent with

the known system L. The tryptophan transport system is predominantly (86%) sodium-independent. The high-affinity system is very specific for tryptophan and shows no transport of any other essential amino acids in the tryptophan transport concentration range. This high-affinity system is expressed at very low levels in fresh monocytes, but undergoes a 10-30 fold induction during macrophage differentiation. This high affinity, tryptophan-selective transport system allows macrophages to take up tryptophan efficiently under conditions of very low substrate concentration, such as can occur at sites of inflammation.

Methods for the isolation of the cDNA that codes for this high affinity tryptophan transport system are described along with methods for the purification of the high affinity transporter. Methods for obtaining and using molecules which interact with the high affinity transporter are also described. Molecules which are obtained by their competitive binding properties with tryptophan for the high affinity transporter tryptophan binding site are also described. Also described are compositions, and methods for using these compositions, which do not competitively interact with tryptophan for the high affinity transporter tryptophan binding site.

#### Brief Description of the Drawings

Figures 1a-c show saturation kinetics for uptake low substrate concentrations (less than 2.5  $\mu\text{M}$ ) of tryptophan transport for the high affinity transporter. Figure 1A is a graph of the  $[v]$  (pmol

Tryptophan/ $10^6/10$  minutes) versus  $[S]$  ( $\mu\text{M}$  Tryptophan). Monocyte-derived macrophages were incubated with varying concentrations between 0 and  $2.5 \mu\text{M}$  of radiolabeled tryptophan, and substrate uptake over 10 min ( $V$ , expressed in  $\text{pmol tryptophan } 10^6 \text{ cells}^{-1} \cdot 10 \text{ min}^{-1}$ ) measured as a function of substrate concentration ( $[S]$ , in  $\mu\text{M}$ ). The inset is an Eadie-Hofstee plot of the uptake data, yielding a calculated  $K_m$  of 230 nM in this experiment. The  $K_m$  values are described in Table 1.

Figure 1B is a graph of the  $[v]$  ( $\text{pmol Tryptophan}/10^6/10$  minutes) versus  $v/[S]$ . The data was derived from an extended titration of tryptophan over a three log range (32 nM to  $64 \mu\text{M}$ ), demonstrating the presence of two transport systems with markedly different affinities (all data taken from a single experiment using the same macrophage preparation). The superimposed lines represent predicted uptake at concentrations of less than  $1 \mu\text{M}$  and greater than  $8 \mu\text{M}$ , based on the  $K_m$  and  $V_{\text{max}}$  values derived from the Lineweaver-Burk plots shown in Figure 1C.

Figure 1C is a Lineweaver-Burk plot for the high affinity data and the low affinity data shown in Figure 1B, demonstrating that each system followed Michaelis-Menten kinetics over the range of concentrations surrounding its  $K_m$  value.

Figures 2A and 2B are graphs of  $1/v$  ( $\text{pmol amino acid } 10^6 \text{ cells}^{-1} \cdot 10 \text{ min}^{-1}$ ) versus  $1/[S]$  ( $\mu\text{M}$ ) for tryptophan transport of leucine and phenylalanine via the low affinity transport system. The affinity constants for uptake of

radiolabeled (Figure 2A) leucine ( $26 \pm 6 \mu\text{M}$ ) and (Figure 2B) phenylalanine ( $29 \pm 2 \mu\text{M}$ ) were determined by saturation kinetics as described in Figure 1.

5        Figure 2C is a saturation graph of tryptophan competition with phenylalanine for uptake. The dotted line shows the predicted inhibition curve calculated from Equation 1 based on the observed  $\text{IC}_{50}$  for the low affinity system L.

10        Figure 3 is a bar graph of the amount of uptake of different amino acids based on the % of tryptophan uptake. Cross-competition studies were performed using radiolabeled tryptophan (125 nM) versus a panel of unlabeled substrates (8 mM each).  
15 All data are expressed as tryptophan uptake relative to controls without added competitor ("CTL").

Figure 4A is a graph of  $[\text{}^3\text{H}]\text{Tryptophan}$  (pmol Tryptophan/ $10^6/10$  minutes) versus  $[\text{S}]$  ( $\mu\text{M}$  Tryptophan) plotted on a semilog plot. Unlabeled 2-aminobicyclo(2,2,1)-heptane-2-carboxylic acid (BCH) (diamonds) or tryptophan (squares) were allowed to compete for uptake with radiolabeled tryptophan (125 nM). The dotted lines show the  
20 predicted inhibition curves calculated from Equation 1 for single isolated systems, based on the observed  $\text{IC}_{50}$  values in experiments of 360 nM and 37  $\mu\text{M}$  for tryptophan and BCH, respectively.

Figure 4B and 4C are graphs of  $V$  versus  $V/[\text{S}]$   
30 at a Tryptophan concentration of greater than 8  $\mu\text{M}$  (Figure 5B) and less than 1  $\mu\text{M}$  (Figure 4C). Saturation kinetics for tryptophan uptake were performed as described with reference to Figure 1,



in the presence (circles) or absence (squares) of 500  $\mu\text{M}$  unlabeled BCH. In the concentration range where system L predominated (greater than 8  $\mu\text{M}$  tryptophan) BCH acted as a competitive inhibitor.

5 However, in the range where the high-affinity system predominated (less than 1  $\mu\text{M}$ ), BCH acted only as a weak non-competitive inhibitor.

Figure 5 is a graph of  $^3\text{H}$  Tryptophan (%control) versus [unlabeled competitor] ( $\mu\text{M}$ ). Unlabeled  
10 phenylalanine (open symbols) was allowed to compete for uptake with radiolabeled tryptophan (125 nM). Equation 1 was used to calculate the predicted inhibition curves (dotted lines) assuming that labeled and unlabeled substrate competed for a  
15 single system, with  $K_i$  in each case equal to the observed  $\text{IC}_{50}$ . This model correctly predicted the behavior of unlabeled tryptophan competing for its own uptake (competition for the high-affinity system, solid diamonds), and of phenylalanine at  
20 low concentrations (competition for system L, open symbols). However, at high concentrations of phenylalanine the observed data departed significantly from that predicted for a single system. Each of the 3 open symbols show data from  
25 separate experiments. A total of 11 experiments were performed using phenylalanine, leucine, tyrosine, or cysteine as competitors, all with similar departure from the predicted single-system kinetics.

30 Figure 6 is a bar graph of the amount of uptake of different amino acids based on the % of tryptophan uptake. Cross-competition studies were performed as described for Figure 3, but using a

concentration of unlabeled competitor ( $4 \mu\text{M}$ )  
predicted to affect only the high-affinity system.

Figure 7 is a graph of percent labeled  
tryptophan ( $250 \text{ nM}$  radiolabelled tryptophan) taken  
up by the high affinity transporter as a function  
of concentration of either unlabelled tryptophan  
(diamonds) or unlabeled 1-methyl tryptophan  
(triangles) of different concentrations. The solid  
line through the diamonds shows the predicted  
inhibition curve if tryptophan competed with a  $K_i$   
equal to the measured  $K_m$  of the high affinity  
system ( $290 \text{ nM}$ ). The solid line through the  
triangles shows the predicted inhibition curve if  
1-methyl tryptophan competed with a  $K_i$  of  $30 \mu\text{M}$ ,  
the measured  $K_m$  of system L.

Figure 8 is a graph of tryptophan uptake  
inhibition at  $25^\circ\text{C}$  (squares) and  $0^\circ\text{C}$  (circles), one  
of three experiments.

Figure 9A and 9B are graphs of  $V$  versus  $V/[S]$   
Peripheral blood monocytes were allowed to  
differentiate in vitro for up to 7 days under the  
influence of MCSF. Saturation kinetics for  
tryptophan uptake were performed as in Figure 1,  
over the range of  $0.032 - 1 \mu\text{M}$  substrate. (Figure  
9A) day 0 (mean  $V_{\text{max}} 0.16 \pm 0.15 \text{ pmol } 10^6 \text{ cells}^{-1} \cdot 10$   
 $\text{min}^{-1}$ ,  $n = 4$  vs. (Figure 9B) day 4-7 (mean  $V_{\text{max}} 2.3$   
 $\pm 0.9$ ,  $n = 6$ ).

Figure 9C is a graph of  $V_{\text{max}}$  (high affinity  
transporter) versus Time (days). This graph  
illustrates the upregulation that takes place  
during macrophage differentiation.

### Detailed Description of the Disclosure

#### *Tryptophan transport Systems in Macrophages*

The known sodium-independent systems are summarized in Kakuda J. Exp. Biol. 1994;196:93-108; 5 McGivan Biochem. J. 1994;299:321-324. There is an IFN $\gamma$ -inducible, high-affinity, tryptophan-selective uptake system in MCSF-derived macrophages. A common feature of both sodium-dependent and sodium-independent systems identified to date is that they 10 all display a relatively modest affinity for substrate ( $K_m$  of even the "high-affinity") systems in the range of 10-30  $\mu$ M, and of the low-affinity systems 100-500  $\mu$ M). This affinity is consistent with the fact that amino acids are normally found 15 *in vivo* in this concentration range. Indeed, given the normal physiologic levels of tryptophan (50  $\mu$ M), even the possibility of an amino acid transport system with nanomolar affinity seems paradoxical, since it would presumably always exist 20 in a saturated state.

However, the local concentration of a substance in tissues may be markedly different from its concentration in the circulation, due to the limited rate of diffusion through the extracellular 25 space (Casciari, et al., 1988 *Cancer Res.* 48, 3905-3909). Data from multicellular spheroid models show that the distance over which even small molecules can be supplied by diffusion in the face of ongoing consumption is limited to 100-200 30 micrometers (Li 1982 *Cancer* 50, 2066-2073). Thus, local concentrations of tryptophan in tissues could be much lower than those in plasma if the rate of consumption is high enough to exceed delivery.

This has been verified empirically *in vivo* by Burke, et al. 1995 *Int. J. Cancer* 60, 115-122. Consumption of tryptophan by activated macrophages can be very high. As a part of their role in host defense, macrophages possess the inducible enzyme, indoleamine 2,3-dioxygenase (IDO), which rapidly and selectively degrades tryptophan in response to infection and inflammation (Taylor and Fong 1991 *FASEB J.* 5, 2516-2522). Activated macrophages degrade tryptophan via IDO at a rate which is 100 times their already high rate of tryptophan consumption by cellular metabolism. Thus, it is readily conceivable that tryptophan degradation could outstrip diffusion-limited substrate delivery in tissues, resulting in very low local tryptophan concentrations within the immediate microenvironment of the macrophage.

A second feature of most amino acid transporters is that they typically accept multiple amino acids. However, there also exist a small number of selective transport systems, which display relative specificity for a particular amino acid. These systems generally target amino acids with a special biologic role, e.g., glutamate transport in neurons, or tyrosine transport in melanosomes. In these specialized settings, the local concentration of the amino acid of interest may be low, and it must compete for uptake with other amino acids present in higher concentration. In this context, a selective system for a particular amino acid would be advantageous.

The data in Figures 1a,b,c indicates that tryptophan transport in macrophages is achieved

through two separate transporters. Uptake kinetics performed at the substrate concentrations of interest (sub-micromolar) revealed a saturable system with extremely high affinity for tryptophan.

5 (Figure 1A) Studies over a more extended range of concentrations revealed that uptake did not follow simple Michaelis-Menton kinetics, but appeared to be due to the presence of two separate transport activities. (Figure 1B and 1C).

10 One system displayed a  $K_m$  value in the range of 20-30 micromolar and a pattern of substrate specificity consistent with system L (Figure 1B).  
*Characterization of the High Affinity Transporter*

The other tryptophan transporter is a high  
15 affinity transport activity with a  $K_m$  value in the nanomolar range ( $K_m=290$  to  $340$  nM,  $n=18$  experiments with 4 donors), which does not correspond to any known tryptophan transporter (Figure 1C and Table 1). The data shown in Figures 3 and 5 indicate that  
20 the transport of tryptophan into macrophages is not completely inhibited by the addition of very high concentrations of similar amino acids. Therefore, macrophages must contain a transporter specific for tryptophan. The data in Figures 4a,b,c confirm  
25 that there are two separate transporters for tryptophan present in macrophages. The low affinity transporter is a non-specific transporter of amino acids because BCH competitively inhibits tryptophan transport (Figure 4B). This type of  
30 transport is similar to system L. The high affinity system is specific for tryptophan because BCH is not able to compete for transport at

concentrations below which the low affinity transporter can function (Figure 4C).

The high affinity transporter is very specific for tryptophan transport. Other amino acids, including neutral amino acids, do not compete with tryptophan for transport into macrophages, by the high affinity system. The data shown in Figure 6 indicate that unlabeled competitor amino acids, used at 4 micromolar, which should significantly inhibit a system with nanomolar affinity, have little impact on the high affinity transporter in transporting tryptophan. System L with a  $K_m$  approximately 30 micromolar for both the competitor amino acids and tryptophan is not affected at 4  $\mu M$  competitor. The uptake of radiolabeled tryptophan (125 nM) was markedly inhibited by 4 micromolar cold tryptophan indicating that 4  $\mu M$  ligand is sufficient to compete with the radiolabeled ligand as long as the transporter is capable of binding the ligand. In contrast, 4  $\mu M$  of any of the tested amino acids (including BCH) was unable to out compete the tryptophan transport.

The 5-hydroxy derivative of tryptophan, which differs from native tryptophan only in a single substitution on the side chain, similarly failed to compete for transport via the high-affinity system (Figure 7), indicating the exquisite specificity of the high-affinity system for tryptophan. Some amino acids showed non-competitive inhibition of the high-affinity system at high concentrations. However, even at millimolar concentrations 20,000 times greater than the  $K_m$  of the high-affinity system, no competing amino acid except tryptophan

itself could fully inhibit uptake of labeled tryptophan.

The data shown in Figure 8 indicates that the higher association of tryptophan, relative to other amino acids, with macrophages is caused by increased relative transport at low concentrations, not simple binding to the macrophage surface. If the observed results are due to simple binding, a reduction in temperature should slow the rate of binding, but the reaction should come to equilibrium. The data in Figure 8 indicate that the amount of tryptophan associated with the macrophages is decreased and it is not in equilibrium, indicating a reduced rate of influx. The  $V_{max}$  of tryptophan transport by the high affinity transporter, normalized by the number of cells, increases when peripheral blood monocytes are induced to differentiate by growth in the presence of macrophage colony stimulating factor (MCSF) Figures 9a,b,c). This increase in velocity is likely caused by an upregulation of the expression of the high affinity tryptophan transporter in macrophages, relative to the progenitor peripheral blood cells.

The high affinity transporter represents an excellent target for the inhibition or activation of tryptophan transport. Tryptophan uptake in macrophages represents a special case in which both high affinity and high selectivity are necessary. At nanomolar substrate concentrations, tryptophan uptake via system L would become inefficient, and it would be rendered even less efficient by the fact that multiple other substrates would compete

for uptake. When Equation 1 is used to predict the uptake of low concentrations of tryptophan via system L alone (50 nM tryptophan, 1 mM total other competing amino acids, and  $K_m$  and  $V_{max}$  values as in Figure 1) uptake is calculated to be  $1.5 \text{ fmol } 10^6 \text{ cells}^{-1} \cdot 10 \text{ min}^{-1}$ . The presence of a selective high-affinity system as described herein would increase tryptophan transport greater than 100-fold, to  $70 \text{ fmol } 10^6 \text{ cells}^{-1} \cdot 10 \text{ min}^{-1}$ . It is postulated that macrophages represent a specialized cell type which due to their own high IDO activity must be prepared to function in settings where the local tryptophan concentration is extremely low. A selective, high-affinity transport system would allow macrophages to continue to take up tryptophan efficiently, even under conditions where other cell types could not. Such a transporter could play an important role in supplying substrate to the IDO enzyme system for degradation, and also in allowing macrophages to compete with other cells for available tryptophan.

One significant feature of the transport system is its selective upregulation during macrophage differentiation. Unlike system L, which is constitutively present in fresh monocytes and only modestly increased in mature macrophages (approximately proportional to the increase in cell size), the high-affinity system undergoes 10- to 30-fold upregulation over the same period. This differentiation step from monocyte to macrophages is also known to produce massive increases in both  $\text{IFN}\gamma$ -inducible IDO activity (Carlin, et al., 1989 *J. Leuk. Biol.* 45, 29-34) and  $\text{IFN}\gamma$ -inducible tryptophanyl-tRNA synthetase activity (Krause, et



al., 1996 *J. Leuk. Biol.* 60, 540-545). Thus, the high-affinity tryptophan transporter is coordinately regulated during macrophage differentiation with two other genes known to be involved in immunoregulated tryptophan metabolism, indicating that the transporter participates in the tryptophan-mediated M $\phi$  immune response.

The following examples examine expression of the high-affinity transporter in macrophages, where it was first identified. However, it is expected to be present in other cell types which may also have specialized needs for tryptophan transport, such as cells of the nervous system, placenta, or blood-brain barrier.

*Isolation of the High Affinity Transporter*  
The transporter can be isolated using standard techniques, based on the presence relative to the cell walls of the macrophages. Examples of techniques that can be used include differential display and macrophage expression libraries which are screened based on the high affinity and selectivity for tryptophan binding, as described in the examples, then purified using traditional chromatography, membrane fractionation, or other standard techniques. Alternatively, the gene encoding the transporter can be cloned as described below, and the gene (or cDNA) expressed to produce a recombinant protein.

*Cloning of the High Affinity Transporter*  
The unusual features of the transporter can be used to clone the transporter. The transporter is unique in its extremely high affinity for tryptophan, and its selectivity for tryptophan over

other amino acids. The previously identified amino acid transporters which accept tryptophan all have affinities in the micromolar-to-milimolar range, and all accept other amino acids which compete with tryptophan for uptake. Thus, under conditions in which the tryptophan concentration is very low (<100 nM) and the total concentration of competing amino acids is very high (greater than 1 mM), cells without the high-affinity transporter would be unable to take up tryptophan efficiently and could not proliferate. However, under these same conditions cells with a high-affinity, tryptophan-selective transporter would still be able to take up tryptophan. Thus, the high-affinity transporter would confer a proliferative advantage under the conditions described.

*Applications for the high affinity transporter with the cloned or purified transporter*

The transporter, or gene, can be used to isolate other transporter proteins, to screen for inhibitors of the transporter, which are useful in altering tryptophan transport or T cell activation, and in screening of patient samples for defects in the transporter, which may be indicative of genetic defects, viral or parasitic infections, or malignancy. The transporter protein is also be useful for making antibodies which can be used in diagnostic assays to measure efficacy of tryptophan transport and the effect of compounds on the transporter, as well as isolation of the transporter.

*Screening for Compounds which Modulate  
Tryptophan Transport Via the High Affinity  
Transporter*

There are three basic mechanisms which can be  
5 used to modulate tryptophan catabolism in cells:  
modulation of IDO concentration or activity;  
modulation of the high affinity tryptophan  
transporter; and modulation of tryptophan  
concentration in the relevant cellular environment.  
10 A number of techniques are known for obtaining  
compounds which can be used to modulate IDO  
expression or activity, tryptophan levels, or the  
activity or expression of the high affinity  
tryptophan transporter, which in turn regulates the  
15 tryptophan levels intracellularly.

Assays for testing compounds for useful  
activity can be based solely on interaction with  
IDO, the high affinity tryptophan transporter, or  
enzymes involved in tryptophan metabolism ("the  
20 enzymes"), or alternatively, the assays can be  
based on interaction with the gene sequence  
encoding the enzymes. For example, antisense which  
binds to the regulatory sequences, and/or to the  
protein encoding sequences can be synthesized using  
25 standard oligonucleotide synthetic chemistry. The  
antisense can be stabilized for pharmaceutical use  
using standard methodology (encapsulation in a  
liposome or microsphere; introduction of modified  
nucleotides that are resistant to degradation or  
30 groups which increase resistance to endonucleases,  
such as phosphorothioates and methylation), then  
screened initially for alteration of enzyme  
activity in transfected or naturally occurring

cells which express the enzyme, then *in vivo* in laboratory animals. Typically, the antisense would inhibit expression. However, sequences which block those sequences which "turn off" synthesis can also  
5 be targeted.

*Random generation of enzyme or enzyme encoding sequence binding molecules.*

Oligonucleotide molecules with a given function, catalytic or ligand-binding, can be  
10 selected for from a complex mixture of random oligonucleotides in what has been referred to as "in vitro genetics" (Szostak, TIBS 19:89, 1992). One synthesizes a large pool of molecules bearing random and defined sequences and subjects that  
15 complex mixture, for example, approximately  $10^{15}$  individual sequences in 100  $\mu\text{g}$  of a 100 nucleotide RNA, to some selection and enrichment process. For example, by repeated cycles of affinity chromatography and PCR amplification of the  
20 molecules bound to the ligand on the column, Ellington and Szostak (1990) estimated that 1 in  $10^{10}$  RNA molecules folded in such a way as to bind a given ligand. DNA molecules with such ligand-binding behavior have been isolated (Ellington and  
25 Szostak, 1992; Bock et al, 1992). Techniques aimed at similar goals exist for small organic molecules, proteins, antibodies and other macromolecules known to those of skill in the art. Screening sets of molecules for a desired activity whether based on  
30 small organic libraries, oligonucleotides, or antibodies is broadly referred to as combinatorial chemistry. Combinatorial techniques are particularly suited for defining binding interactions between molecules.

Using methodology well known to those of skill in the art, in combination with various combinatorial libraries, one can isolate and characterize those compounds which bind to or  
5 interact with the desired target. The relative binding affinity of these compounds can be compared and optimum compounds identified using competitive binding studies which are well known to those of skill in the art.

10 Screening molecules similar to tryptophan for inhibition of tryptophan binding or transport is a method of isolating desired compounds. The high affinity tryptophan transporter is highly specific for tryptophan transport.

15 Molecules isolated which inhibit tryptophan transport can either be competitive inhibitors of the high affinity tryptophan transporter or non-competitive inhibitors. In one embodiment the molecules are competitive inhibitors of tryptophan  
20 transport by the high affinity transporter. It is preferred that competitive inhibitors of tryptophan transport via the high affinity transporter do not get transported via the low affinity transporter. It is most preferred that competitive inhibitors of  
25 tryptophan transport via the high affinity transport system do not get transported via either the high affinity or low affinity transporters. This prevents unwanted intracellular buildup of tryptophan analogs.

30 In another embodiment the inhibitors of tryptophan transport by the high affinity transporter are non-competitive inhibitors of tryptophan transport. One type of non-competitive

inhibitor will cause allosteric rearrangements which prevent the transporter from binding or transporting tryptophan. Another type of non-competitive inhibitor of tryptophan transport by the high affinity transporter binds the high affinity transporter in a place other than the tryptophan binding site. However, it prevents tryptophan from accessing the tryptophan binding site because of steric hinderance.

10 Non-competitive inhibitors specific for the high affinity tryptophan transporter are preferred.

*Computer assisted drug design*

Computer modeling technology allows visualization of the three-dimensional atomic structure of a selected molecule and the rational design of new compounds that will interact with the molecule. The three-dimensional construct typically depends on data from x-ray crystallographic analyses or NMR imaging of the selected molecule. The molecular dynamics require force field data. The computer graphics systems enable prediction of how a new compound will link to the target molecule and allow experimental manipulation of the structures of the compound and target molecule to perfect binding specificity. Prediction of what the molecule-compound interaction will be when small changes are made in one or both requires molecular mechanics software and computationally intensive computers, usually coupled with user-friendly, menu-driven interfaces between the molecular design program and the user.

Examples of molecular modelling systems are the CHARMM and QUANTA programs, Polygen

Corporation, Waltham, MA. CHARMM performs the energy minimization and molecular dynamics functions. QUANTA performs the construction, graphic modelling and analysis of molecular structure. QUANTA allows interactive construction, modification, visualization, and analysis of the behavior of molecules with each other.

A number of articles review computer modeling of drugs interactive with specific proteins, such as Rotivinen, et al., 1988 *Acta Pharmaceutica Fennica* 97, 159-166; Ripka, *New Scientist* 54-57 (June 16, 1988); McKinaly and Rossmann, 1989 *Annu. Rev. Pharmacol. Toxicol.* 29, 111-122; Perry and Davies, OSAR: Quantitative Structure-Activity Relationships in Drug Design pp. 189-193 (Alan R. Liss, Inc. 1989); Lewis and Dean, 1989 *Proc. R. Soc. Lond.* 236, 125-140 and 141-162; and, with respect to a model enzyme for nucleic acid components, Askew, et al., 1989 *J. Am. Chem. Soc.* 111, 1082-1090. Other computer programs that screen and graphically depict chemicals are available from companies such as BioDesign, Inc., Pasadena, CA., Allelix, Inc, Mississauga, Ontario, Canada, and Hypercube, Inc., Cambridge, Ontario. Although these are primarily designed for application to drugs specific to particular proteins, they can be adapted to design of drugs specific to regions of DNA or RNA, once that region is identified.

Although described above with reference to design and generation of compounds which could alter binding, one could also screen libraries of known compounds, including natural products or

synthetic chemicals, and biologically active materials, including proteins, for compounds which alter substrate binding or enzymatic activity.

*Generation of nucleic acid regulators*

5       Nucleic acid molecules containing the 5' regulatory sequences of the enzyme or transporter genes can be used to regulate or inhibit gene expression *in vivo*. Vectors, including both plasmid and eukaryotic viral vectors, may be used  
10 to express a particular recombinant 5' flanking region-gene construct in cells depending on the preference and judgment of the skilled practitioner (see, e.g., Sambrook et al., Chapter 16). Furthermore, a number of viral and nonviral vectors  
15 are being developed that enable the introduction of nucleic acid sequences *in vivo* (see, e.g., Mulligan, 1993 *Science*, 260, 926-932; United States Patent No. 4,980,286; United States Patent No. 4,868,116; incorporated herein by reference).  
20 Nucleic acid can be encapsulated in cationic liposomes which can be injected intravenously into a mammal. This system has been used to introduce DNA into the cells of multiple tissues of adult mice, including endothelium and bone marrow (see,  
25 e.g., Zhu et al., 1993 *Science* 261, 209-211).

      The 5' flanking sequences of the enzyme gene can also be used to inhibit the expression of the enzyme. For example, an antisense RNA of all or a portion of the 5' flanking region of the enzyme  
30 gene can be used to inhibit expression of the enzyme *in vivo*. Expression vectors (e.g., retroviral expression vectors) are already available in the art which can be used to generate



an antisense RNA of a selected DNA sequence which is expressed in a cell (see, e.g., U.S. Patent No. 4,868,116; U.S. Patent No. 4,980,286).

Accordingly, DNA containing all or a portion of the sequence of the 5' flanking region of the enzyme gene can be inserted into an appropriate expression vector so that upon passage into the cell, the transcription of the inserted DNA yields an antisense RNA that is complementary to the mRNA transcript of the enzyme gene normally found in the cell. This antisense RNA transcript of the inserted DNA can then base-pair with the normal mRNA transcript found in the cell and thereby prevent the mRNA from being translated. It is of course necessary to select sequences of the 5' flanking region that are downstream from the transcriptional start sites for the enzyme gene to ensure that the antisense RNA contains complementary sequences present on the mRNA.

Antisense RNA can be generated *in vitro* also, and then inserted into cells. Oligonucleotides can be synthesized on an automated synthesizer (e.g., Model 8700 automated synthesizer of Milligen-Bioscience, Burlington, MA or ABI Model 380B). In addition, antisense deoxyoligonucleotides have been shown to be effective in inhibiting gene transcription and viral replication (see e.g., Zamecnik et al., 1978 *Proc. Natl. Acad. Sci. USA* 75, 280-284; Zamecnik et al., 1986 *Proc. Natl. Acad. Sci.*, 83, 4143-4146; Wickstrom et al., 1988 *Proc. Natl. Acad. Sci. USA* 85, 1028-1032; Crooke, 1993 *FASEB J.* 7, 533-539. Inhibition of expression of a gene by antisense oligonucleotides is possible

if the antisense oligonucleotides contain modified nucleotides (see, e.g., Offensperger et al., 1993 *EMBO J.* 12, 1257-1262 (in vivo inhibition of duck hepatitis B viral replication and gene expression by antisense phosphorothioate oligodeoxynucleotides); Rosenberg et al., PCT WO 93/01286 (synthesis of sulfurthioate oligonucleotides); Agrawal et al., 1988 *Proc. Natl. Acad. Sci. USA* 85, 7079-7083 (synthesis of antisense oligonucleoside phosphoramidates and phosphorothioates to inhibit replication of human immunodeficiency virus-1); Sarin et al., 1989 *Proc. Natl. Acad. Sci. USA* 85, 7448-7794 (synthesis of antisense methylphosphonate oligonucleotides); Shaw et al., 1991 *Nucleic Acids Res* 19, 747-750 (synthesis of 3' exonuclease-resistant oligonucleotides containing 3' terminal phosphoroamidate modifications); incorporated herein by reference).

20       The sequences of the 5' flanking region of enzyme gene can also be used in triple helix (triplex) gene therapy. Oligonucleotides complementary to gene promoter sequences on one of the strands of the DNA have been shown to bind promoter and regulatory sequences to form local triple nucleic acid helices which block transcription of the gene (see, e.g., 1989 Maher et al., *Science* 245, 725-730; Orson et al., 1991 *Nucl. Acids Res.* 19, 3435-3441; Postal et al., 1991 *Proc. Natl. Acad. Sci. USA* 88, 8227-8231; Cooney et al., 1988 *Science* 241, 456-459; Young et al., 1991 *Proc. Natl. Acad. Sci. USA* 88, 10023-10026; Duval-Valentin et al., 1992 *Proc. Natl. Acad. Sci. USA*

89, 504-508; 1992 Blume et al., *Nucl. Acids Res.*  
20, 1777-1784; 1992 Grigoriev et al., *J. Biol.*  
*Chem.* 267, 3389-3395.

Both theoretical calculations and empirical  
5 findings have been reported which provide guidance  
for the design of oligonucleotides for use in  
oligonucleotide-directed triple helix formation to  
inhibit gene expression. For example,  
oligonucleotides should generally be greater than  
10 14 nucleotides in length to ensure target sequence  
specificity (see, e.g., Maher et al., (1989);  
Grigoriev et al., (1992)). Also, many cells avidly  
take up oligonucleotides that are less than 50  
nucleotides in length (see e.g., Orson et al.,  
15 (1991); Holt et al., 1988 *Mol. Cell. Biol.* 8, 963-  
973; Wickstrom et al., 1988 *Proc. Natl. Acad. Sci.*  
*USA* 85, 1028-1032). To reduce susceptibility to  
intracellular degradation, for example by 3'  
exonucleases, a free amine can be introduced to a  
20 3' terminal hydroxyl group of oligonucleotides  
without loss of sequence binding specificity (Orson  
et al., 1991). Furthermore, more stable triplexes  
are formed if any cytosines that may be present in  
the oligonucleotide are methylated, and also if an  
25 intercalating agent, such as an acridine  
derivative, is covalently attached to a 5' terminal  
phosphate (e.g., via a pentamethylene bridge);  
again without loss of sequence specificity (Maher  
et al., (1989); Grigoriev et al., (1992)).

30 Methods to produce or synthesize  
oligonucleotides are well known in the art. Such  
methods can range from standard enzymatic digestion  
followed by nucleotide fragment isolation (see

e.g., Sambrook et al., Chapters 5, 6) to purely synthetic methods, for example, by the cyanoethyl phosphoramidite method using a Milligen or Beckman System 1Plus DNA synthesizer (see also, Ikuta et al., in *Ann. Rev. Biochem.* 1984 53, 323-356 (phosphotriester and phosphite-triester methods); Narang et al., in *Methods Enzymol.*, 65, 610-620 (1980) (phosphotriester method). Accordingly, DNA sequences of the 5' flanking region of the enzyme gene described herein can be used to design and construct oligonucleotides including a DNA sequence consisting essentially of at least 15 consecutive nucleotides, with or without base modifications or intercalating agent derivatives, for use in forming triple helices specifically within the 5' flanking region of a enzyme gene in order to inhibit expression of the gene.

In some cases it may be advantageous to insert enhancers or multiple copies of the regulatory sequences into an expression system to facilitate screening of methods and reagents for manipulation of expression.

#### *Preparation of Protein Fragments or Amino Acid Analogs*

Compounds which are effective for blocking binding of the transporter or IDO can also consist of protein fragments, expressed recombinantly and cleaved by enzymatic digest or expressed from a sequence encoding a peptide of less than the full length protein, or tryptophan analogs which compete with tryptophan for binding and/or uptake by the high affinity tryptophan transporter. It is a routine matter to make appropriate protein

fragments, and test for inhibition of activity of the protein in the presence of the fragments. The preferred fragments are of human origin, in order to minimize potential immunological response. The peptides can be as short as five to eight amino acids in length and are easily prepared by standard techniques. They can also be modified to increase in vivo half-life, by chemical modification of the amino acids or by attachment to a carrier molecule or inert substrate. The peptides can also be conjugated to a carrier protein such as keyhole limpet hemocyanin by its N-terminal cysteine by standard procedures such as the commercial Imject kit from Pierce Chemicals or expressed as a fusion protein, which may have increased efficacy. As noted above, the peptides can be prepared by proteolytic cleavage of the proteins, or, preferably, by synthetic means. These methods are known to those skilled in the art. An example is the solid phase synthesis described by J. Merrifield, 1964 *J. Am. Chem. Soc.* 85, 2149, used in U.S. Patent No. 4,792,525, and described in U.S. Patent No. 4,244,946, wherein a protected alpha-amino acid is coupled to a suitable resin, to initiate synthesis of a peptide starting from the C-terminus of the peptide. Other methods of synthesis are described in U.S. Patent No. 4,305,872 and 4,316,891. These methods can be used to synthesize peptides having identical sequence to the proteins described herein, or substitutions or additions of amino acids, which can be screened for activity as described above.

The peptide can also be administered as a pharmaceutically acceptable acid- or base- addition salt, formed by reaction with inorganic acids such as hydrochloric acid, hydrobromic acid, perchloric acid, nitric acid, thiocyanic acid, sulfuric acid, and phosphoric acid, and organic acids such as formic acid, acetic acid, propionic acid, glycolic acid, lactic acid, pyruvic acid, oxalic acid, malonic acid, succinic acid, maleic acid, and fumaric acid, or by reaction with an inorganic base such as sodium hydroxide, ammonium hydroxide, potassium hydroxide, and organic bases such as mono-, di-, trialkyl and aryl amines and substituted ethanolamines.

Peptides containing cyclopropyl amino acids, or amino acids derivatized in a similar fashion, can also be used. These peptides retain their original activity but have increased half-lives *in vivo*. Methods known for modifying amino acids, and their use, are known to those skilled in the art, for example, as described in U.S. Patent No. 4,629,784 to Stammer.

#### *Pharmaceutical Compositions*

Compounds which alter enzyme activity are preferably administered in a pharmaceutically acceptable vehicle. Suitable pharmaceutical vehicles are known to those skilled in the art. For parenteral administration, the compound will usually be dissolved or suspended in sterile water or saline.

#### *Generation of Transgenic Animals for Screening*

With the knowledge of the cDNA encoding the high affinity tryptophan transporter and regulatory

sequences regulating expression thereof, it is possible to generate transgenic animals, especially rodents, for testing the compounds which can alter enzyme expression, translation or function in a  
5 desired manner.

There are basically two types of animals which are useful: those not expressing the high affinity transporter, and those which overexpress the high affinity transporter, either in those tissues which  
10 already express the protein or in those tissues where only low levels are naturally expressed. The animals in the first group are preferably made using techniques that result in "knocking out" of the gene for enzyme, although in the preferred case  
15 this will be incomplete, either only in certain tissues, or only to a reduced amount. These animals are preferably made using a construct that includes complementary nucleotide sequence to the enzyme gene, but does not encode functional enzyme,  
20 and is most preferably used with embryonic stem cells to create chimeras. Animals which are heterozygous for the defective gene can also be obtained by breeding a homozygote normal with an animal which is defective in production of enzyme.

25 The animals in the second group are preferably made using a construct that includes an unregulated promoter or one which is modified to increase expression as compared with the native promoter. The regulatory sequences for the enzyme gene can be  
30 obtained using standard techniques based on screening of an appropriate library with the cDNA encoding enzyme. These animals are most preferably made using standard microinjection techniques.

These manipulations are performed by insertion of cDNA or genomic DNA into the embryo using microinjection or other techniques known to those skilled in the art such as electroporation, as  
5 described below. The DNA is selected on the basis of the purpose for which it is intended: to inactivate the gene or to overexpress the gene. The enzyme encoding gene can be modified by homologous recombination with a DNA for a defective  
10 enzyme, such as one containing within the coding sequence an antibiotic marker, which can then be used for selection purposes.

Animals suitable for transgenic experiments can be obtained from standard commercial sources.  
15 These include animals such as mice and rats for testing of genetic manipulation procedures, as well as larger animals such as pigs, cows, sheep, goats, and other animals that have been genetically engineered using techniques known to those skilled  
20 in the art. The procedures for manipulation of the embryo and for microinjection of DNA are described in detail in Hogan et al. Manipulating the mouse embryo, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1986), the teachings of which are  
25 incorporated herein. These techniques are readily applicable to embryos of other animal species, and, although the success rate is lower, it is considered to be a routine practice to those skilled in this art. Methods for the culturing of  
30 ES cells and the subsequent production of transgenic animals, the introduction of DNA into ES cells by a variety of methods such as electroporation, calcium phosphate/DNA



precipitation, and direct injection are described in detail in Teratocarcinomas and embryonic stem cells, a practical approach, ed. E.J. Robertson, (IRL Press 1987), the teachings of which are

5 incorporated herein. Transfection is carried out by one of several methods described in detail in Lovell-Badge, in Teratocarcinomas and embryonic stem cells, a practical approach, ed. E.J. Robertson, (IRL Press 1987) or in Potter et al

10 Proc. Natl. Acad. Sci. USA 81, 7161 (1984). Calcium phosphate/DNA precipitation, direct injection, and electroporation are the preferred methods. DNA molecules introduced into ES cells can also be integrated into the chromosome through

15 the process of homologous recombination, described by Capecchi, (1989). Direct injection results in a high efficiency of integration. Desired clones are identified through PCR of DNA prepared from pools of injected ES cells. Positive cells within the

20 pools are identified by PCR subsequent to cell cloning (Zimmer and Gruss, Nature 338, 150-153 (1989)).

Once the transgenic animals are identified, lines are established by conventional breeding and

25 used as the donors for tissue removal and implantation using standard techniques for implantation into humans.

#### *Gene Therapy*

Altered levels of transporter can also be

30 achieved using gene therapy, either to administer nucleotide molecules which inhibit transporter activity, or to increase transporter activity either through direct alteration of activity, for

example by increasing substrate binding affinity,  
or through overexpression.

#### Examples

The following methods and materials were used  
5 in the examples.

*Materials.* Recombinant human macrophage  
colony-stimulating factor (MCSF) was the gift of  
Genetics Institute, Cambridge MA. Recombinant  
human interferon- $\gamma$  (IFN $\gamma$ ) was the gift of Genentech,  
10 South San Francisco, CA. Radiolabeled  
[ $^3$ H]tryptophan (21 Ci/mmol) was obtained from  
Amersham USA. All preparations were adjusted with  
their respective unlabeled amino acids to a  
specific activity of 20 Ci/mmol before use.  
15 Unlabeled amino acids and all other reagents were  
obtained from Sigma unless otherwise specified.  
Tyrosine and other sparingly-soluble amino acids  
were dissolved in 0.1 M NaOH prior to dilution.

*Monocyte isolation and culture.* Human  
20 peripheral blood monocytes were isolated from  
healthy volunteer donors by leukocytapheresis and  
counterflow centrifugal elutriation, following  
appropriate informed consent under a protocol  
approved by our Institutional Review Board.  
25 Monocytes of greater than 95% purity by cell  
surface markers (Munn and Armstrong 1993 *Cancer*  
*Res.* 53, 2603-2613) were cultured as described by  
Munn and Cheung 1989 *J. Exp. Med.* 170, 511-526, for  
7 days in the presence of MCSF (200 U/ml). The  
30 monocytic leukemia lines THP-1 and U-937 were  
obtained from the American Type Culture Collection,  
Rockville, MD.

*Uptake measurements.* Single cell suspensions were obtained by treating macrophage monolayers with 2 mM EDTA in Hanks balanced salt solution for 15 minutes at room temperature. Cells were washed  
5 twice in Tris-choline buffer (150 mM choline chloride, 10 mM tris, pH 7.4), suspended in Tris-choline at between one and  $2 \times 10^6$  cells/ml, and 100  $\mu$ l/well added to 96 well microtiter plates. Titrations of radiolabeled amino acids were then  
10 transferred to the assay plate and uptake allowed to proceed for 10 minutes (the linear range). At the end of the assay period, wells were harvested simultaneously onto glass-fiber filters and washed vigorously for 30 seconds with phosphate buffered  
15 saline solution using a Tomtec 96 well parallel harvester. Nonspecific binding of radioactivity to the filters (based on wells without cells) was typically less than 10% of the total signal, and was subtracted from each data point. All assays  
20 were performed in triplicate; where error bars are not shown the SD between replicates was less than 10%. In all assays, the uptake rate (V) was normalized per  $1 \times 10^6$  cells (expressed as  $\text{pmol } 10^6 \text{ cells}^{-1} \cdot 10 \text{ min}^{-1}$ ). Normalization to milligrams  
25 protein was considered less informative because protein content can change markedly during macrophage differentiation, independently of other functional attributes.

*Analysis of saturation kinetics.* Uptake  
30 kinetics were analyzed using an Eadie-Hofstee transformation ( $V/[S]$  vs.  $V$ ) to identify linear concentration ranges for each transporter. Data from these two ranges were then analyzed separately

using double-reciprocal (Lineweaver-Burk,  $1/[S]$  vs.  $1/V$ ) plots to determine  $K_m$  and  $V_{max}$ . In all cases, comparable results were obtained if these parameters were estimated from the Eadie-Hofstee plots. Regression analysis was performed using the Microsoft Excel spreadsheet program. Kinetic parameters were calculated on a minimum of 4-6 points, and were considered reliable if the correlation coefficient of the regression line was greater than 0.95.

For competitive inhibition studies, the  $K_i$  value for each competitor was estimated by fitting the measured inhibition curve to the formula in Equation 1 (Cheng and Prusoff 1973, *Biochem. Pharmacol.* 22, 3099-3108).

EQUATION 1:

$$V_i = \frac{V_{max} \cdot [S]}{K_m \cdot \left(1 + \frac{[I]}{K_i}\right) + [S]}$$

where  $[S]$  is the concentration of labeled substrate,  $[I]$  is the concentration of unlabeled inhibitor,  $V_i$  is the observed rate of uptake in the presence of inhibitor,  $K_i$  is the putative affinity constant of the inhibitor for the transporter, and  $K_m$  and  $V_{max}$  have their customary meanings. This equation assumes a single transport system and so does not fully model the situation in macrophages, where two transporters are present. However, the affinity constants of the two systems differed so widely (100-fold) that the data closely fit a single-system model at substrate concentrations surrounding the respective  $K_m$  values.

Example 1:       Tryptophan transport is sodium-independent and occurs via two transport systems.

Monocyte derived macrophages were incubated  
5 with radiolabeled tryptophan (125 nM) for 2, 4, 6 or 10 minutes, either in buffered saline solution (150 mM NaCl) or buffered choline chloride. The majority of tryptophan uptake is sodium-independent. Uptake in the absence of sodium was  
10 86  $\pm$ 6% of uptake in saline, n=4 Therefore all subsequent assays were performed in the absence of sodium.

Saturation kinetics at low substrate concentrations (less than 2.5  $\mu$ M) indicated that  
15 the tryptophan transport system is a saturable system with very high affinity (Figures 1A). Studies over an extended range of concentrations revealed that tryptophan uptake did not follow simple Michaelis-Menten kinetics. Analyzing the  
20 data with Eadie-Hofstee ( $V/[s]$  vs.  $V$ ) plots suggested the presence of two transport systems, as indicated by the non-linear nature of the transformed data (Figure 1B). The transport kinetics were analyzed separately at high (8-64  $\mu$ M)  
25 and low (less than 1  $\mu$ M) substrate concentrations, using Lineweaver-Burk plots (Figure 1C). Individually the data indicated two independent, saturable transport systems, the first with a low affinity ( $K_m$  of 20-30  $\mu$ M, which is in the usual  
30 range for previously described "high-affinity" amino acid transporters (Sanches del Pino, et al., 1995, *J. Biol. Chem.* 270, 14913-14918; Mokrzan, et al., 1995, *J. Pharmacol. Exp. Ther.* 272, 1277-1284;

Low, et al., 1993, *J. Cell. Physiol.* 156, 626-634;  
Prasad, et al., 1994, *Endocrinol.* 134, 574-581; and  
Low, et al., 1994, *J. Biol. Chem.* 269, 32098-  
32103)), and the second system with a very high  
5 affinity ( $K_m$  of approximately 300 nM). When the  $K_m$   
and  $V_{max}$  constants obtained from these separate  
analyses were employed with the Michaelis-Menten  
equation to generate Theoretical predicted uptake  
curves for each system were generated, using the  $K_m$   
10 and  $V_{max}$  values derived from the independent  
analysis of the low affinity data set and the high  
affinity data set. The observed data over the  
range of concentrations surrounding each  $K_m$  fit  
well to the generated curves (the predicted  
15 regression lines are superimposed on Figure 1B).  
Therefore, tryptophan uptake in macrophages was  
modeled best as two independent transport systems,  
each following classical Michaelis-Menten kinetics  
but with markedly different affinities for  
20 substrate.

Table I summarizes the high-affinity system in  
human macrophages and two human macrophage-like  
cell lines, THP-1 and U-937. Human macrophages were  
allowed to differentiate for seven days under the  
25 influence of macrophage colony stimulating factor  
(MCSF). Macrophages and cell lines were assayed  
for tryptophan uptake, and the  $K_m$  value was  
determined for the range of substrate  
concentrations 32 nM - 1  $\mu$ M.

**Table 1: Presence of the high-affinity tryptophan transporter in macrophages and macrophage-like cell lines.**

Cell type	K <sub>m</sub> (μM)	Experiments (n)
macrophages	0.29 ± 0.16	18
THP-1	0.25 ± 0.12	11
U-937	0.34 ± 0.33	3

**Example 2: Uptake via the lower-affinity system is consistent with system L.**

Of the known sodium-independent transport systems only system L accepts tryptophan with low-micromolar affinity (reported affinity as high as K<sub>m</sub>=8-30 μM). This was consistent with the values observed for the lower-affinity system (K<sub>m</sub> = 27 ± 4 μM, n=4, Figure 1) herein described. Leucine and phenylalanine, as shown in Figures 2a,b,c, which are both known substrates for system L, were transported via the low affinity system with comparable affinity. Tryptophan competed with phenylalanine for uptake via this system, with a K<sub>i</sub> value similar to the K<sub>m</sub> value for its own uptake via the lower-affinity system (Figures 1B and 1C). Cross-competition experiments showed that tryptophan transport could be at least partially inhibited by a number of other neutral amino acids, which is also consistent with a contribution of system L in tryptophan transport.

BCH is a substrate which is used as the model substrate for system L transport. Figure 3

indicates that tryptophan transport is inhibited by BCH, but not by charged amino acids. Thus, the lower-affinity transport system present in macrophages displayed multiple features consistent with system L, and is very likely system L or a new transport system with characteristics much like those of system L.

**Example 3:** Uptake via the high-affinity system is distinct from system L and very specific for tryptophan.

Uptake via system L was distinguished from uptake via the previously unidentified high-affinity system. BCH was used to selectively compete for uptake via system L. As shown in Figure 4A, the  $IC_{50}$  for inhibition of tryptophan transport by BCH was approximately 100-fold greater than the  $IC_{50}$  for inhibition by tryptophan itself. Using Equation 1, the data for BCH fit well to a single system, competitive-inhibition model with a  $K_i$  equal to the observed  $IC_{50}$  of 37  $\mu M$ . In contrast, inhibition by unlabeled tryptophan fit to a much higher affinity model ( $K_i = IC_{50} = 360$  nM in the experiment shown), and BCH showed no evidence of competition for this system (as indicated by the lack of inhibition at competitor concentrations less than 1  $\mu M$ ).

The saturation kinetics of tryptophan transport were compared in the presence or absence of BCH. BCH was found to act as a competitive inhibitor over the range of substrate concentrations affected by system L, but it interacted only weakly ( $IC_{50} > 500$   $\mu M$ ) with the high-affinity system (Figure 4C).



More importantly, the interaction between BCH and the high affinity system was strictly non-competitive. BCH did not compete with tryptophan for transport via the high-affinity system. Similar results were obtained for leucine and phenylalanine, indicating that leucine and phenylalanine do not compete with tryptophan for transport by the high affinity system. Thus, while tryptophan competed with multiple substrates for transport by system L, the high-affinity component of tryptophan transport is selective for tryptophan.

The data represented in Figure 2 indicated that even at 8000  $\mu\text{M}$  competitor, tryptophan was not fully inhibited from being transported. Since tryptophan competed with these other substrates at approximately 30  $\mu\text{M}$  (Figures 2 and 4), then a single system composed of system L under these conditions would have less than 1 % of the tryptophan being transported. Since there are two transport systems either the transport systems have the same specificity or different. If the high affinity transport system had specificity requirements similar to system L, then 8000  $\mu\text{M}$  competitor should have reduced tryptophan transport to below 1 % of the control, as if there was only one system. Therefore, this data (Figures 2, 3, 4) also indicated that the transport of tryptophan is occurring via different pathways, one of which is highly specific for tryptophan, relative to other amino acids.

Extended titrations were performed using several unlabeled competitors (leucine,

phenylalanine, tyrosine, cysteine, and BCH) (Figure 3). Phenylalanine was identified as the most efficient competitor, and data for this representative substrate are shown in Figure 4.

5 Like BCH, phenylalanine displayed no detectable competition for the high-affinity system (i.e., no inhibition at competitor concentrations less than 1  $\mu\text{M}$ ). Based on the  $\text{IC}_{50}$ , phenylalanine was predicted to compete with tryptophan with a  $K_i$  of

10 approximately 10  $\mu\text{M}$ . However, at high competitor concentrations the observed inhibition departed markedly from that predicted for a single system. Instead, tryptophan uptake continued at a rate significantly higher than expected, suggesting the

15 presence of an additional transporter not subject to competition by phenylalanine. Titrations of leucine, tyrosine, cysteine, and BCH all showed similar patterns, with even less interaction with the tryptophan-selective component, which was

20 consistent with the results shown in Figure 3.

The cross-competition studies shown in Figure 3 were repeated using unlabeled competitors at a concentration of 4  $\mu\text{M}$  rather than 8000  $\mu\text{M}$ . Based on Equation 1, this concentration was predicted to

25 significantly inhibit the higher-affinity system (80% inhibition) but have little impact (less than 10% inhibition) on the lower-affinity system. As shown in Figure 6, tryptophan uptake was markedly inhibited by 4  $\mu\text{M}$  unlabeled tryptophan, but BCH and

30 all other substrates tested had minimal effect. Thus, when tested in isolation, the high-affinity system displayed a pattern of substrate specificity entirely different from that of system L or any of

the known sodium-independent transport systems, and appeared highly selective for tryptophan.

Example 4:       Tryptophan does not compete with  
                  other substrates for the high-  
5                   affinity system.

The data presented in Examples 1-3 is not consistent with a single system that has markedly higher affinity for tryptophan because tryptophan was not able to preferentially compete for uptake  
10 over other substrates. An additional study in which unlabeled tryptophan was allowed to compete for uptake of radiolabeled leucine, phenylalanine, or tryptophan, all at 125 nM shows that tryptophan competed with labeled leucine or phenylalanine only  
15 for the shared system L, and only with the expected affinity ( $K_i = 30 \mu\text{M}$ ). There was no detectable high-affinity inhibition of phenylalanine or leucine uptake by tryptophan. In contrast, tryptophan competed for its own uptake with the  
20 predicted high affinity. Therefore, the data supported the existence of two separate transporters, with the high-affinity system being selective for tryptophan.

No other amino acid transporter accepting  
25 tryptophan has the same very high degree of specificity. As shown by Figure 7, comparing the amount of labeled tryptophan (250 nM radiolabelled tryptophan) taken up by the high affinity transporter as a function of concentration of  
30 either unlabelled tryptophan or unlabeled 1-methyl tryptophan at different concentrations. The solid line through the diamonds shows the predicted inhibition curve if tryptophan competed with a  $K_i$

equal to the measured  $K_m$  of the high affinity system (290 nM). The solid line through the triangles shows the predicted inhibition curve if 1-methyl tryptophan competed with a  $K_i$  of 30  $\mu M$ ,  
5 the measured  $K_m$  of system L. There was no competition by 1-methyl tryptophan for the high affinity system.

The same type of experiment was done with D-tryptophan, serotonin, 5-hydroxy tryptophan and N-  
10 acetyl tryptophan. These additional substrates also did not compete with tryptophan for the high-affinity system.

**Example 5: High-affinity tryptophan uptake reflects transmembrane transport.**

15 To distinguish between transmembrane transport and binding of tryptophan to a high-affinity cell-surface receptor, the uptake of tryptophan at 25°C and 0°C was compared. As shown in Figure 8, the rate of tryptophan accumulation was reduced by 90%  
20 at 0°C, and this difference remained constant over an extended assay period (30 min). Thus, the accumulation of cell-associated tryptophan was consistent with transmembrane transport rather than surface-receptor binding.

25 **Example 6: The high-affinity system is induced during macrophage differentiation.**

Peripheral blood monocytes undergo many functional changes as they differentiate into macrophages. The high-affinity tryptophan  
30 transporter was regulated during macrophage differentiation. For these experiments, transporter expression was defined as the  $V_{max}$  for the high affinity component derived from Eadie-

Hofstee plots (Figure 2). As shown in Figures 9a,b,c, the high affinity system underwent a 10-30 fold upregulation in  $V_{max}$  during macrophage differentiation. By comparison, the system L  
5 component underwent only a 2- to 3-fold induction over the same period (from  $14 \pm 8$  to  $27 \pm 4$  pmol  $10^6$  cells<sup>-1</sup> 10 min<sup>-1</sup>,  $n = 4$ ). Thus, the high-affinity system was markedly and selectively induced during macrophage differentiation.

1. A high affinity transport system for tryptophan having a  $K_m$  of between approximately 130 and 450 nM, which does not exhibit competitive inhibition by any other essential amino acids, and which is inducible during macrophage differentiation.
2. An isolated nucleotide molecule encoding a high affinity transport system for tryptophan having a  $K_m$  of between approximately 130 and 450 nM, which does not exhibit competitive inhibition by any other essential amino acids, and which is inducible during macrophage differentiation.
3. An animal in which expression is altered of a high affinity transport system for tryptophan having a  $K_m$  of between approximately 130 and 450 nM, which does not exhibit competitive inhibition by any other essential amino acids, and which is inducible during macrophage differentiation.

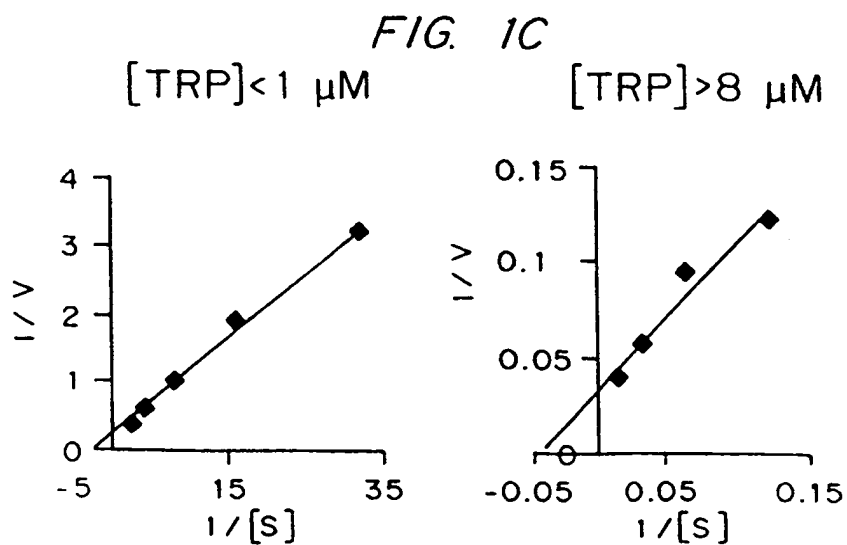
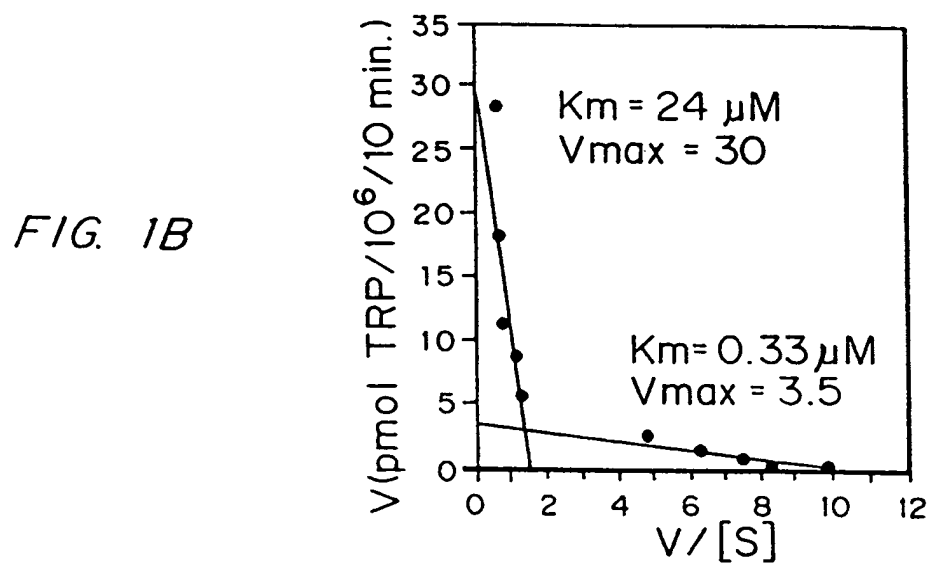
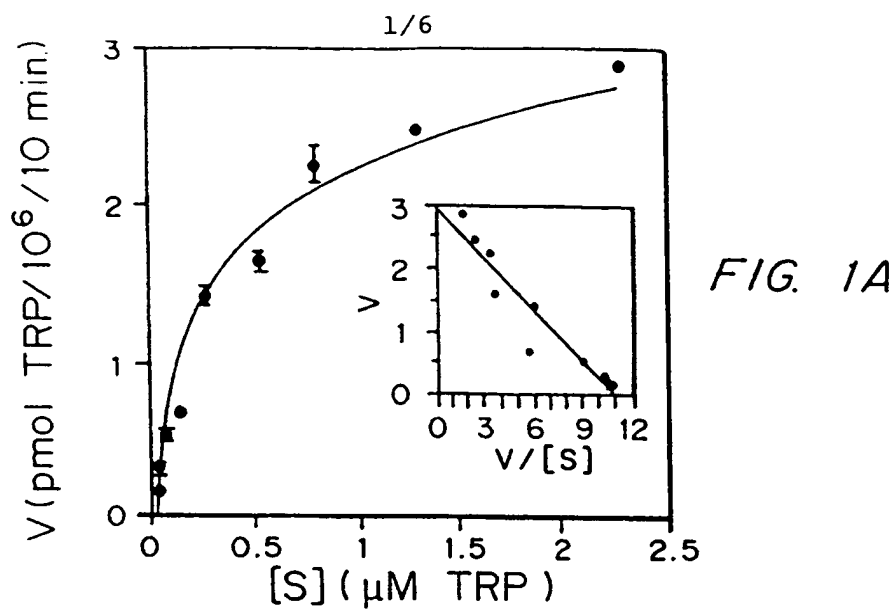


FIG. 2A

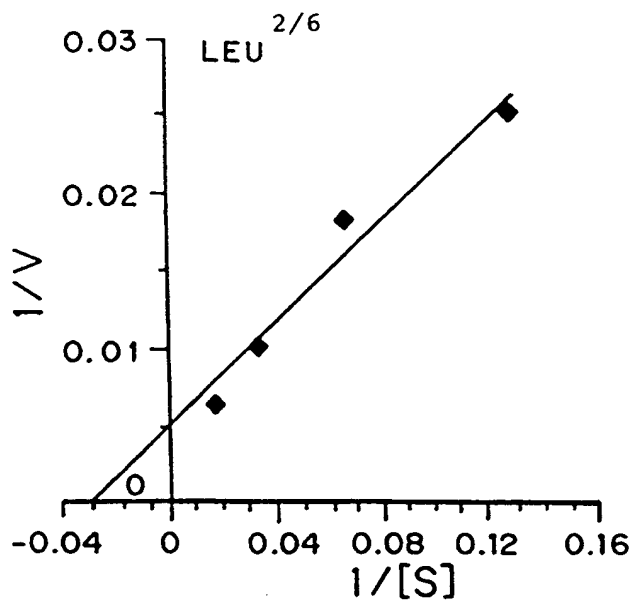


FIG. 2B

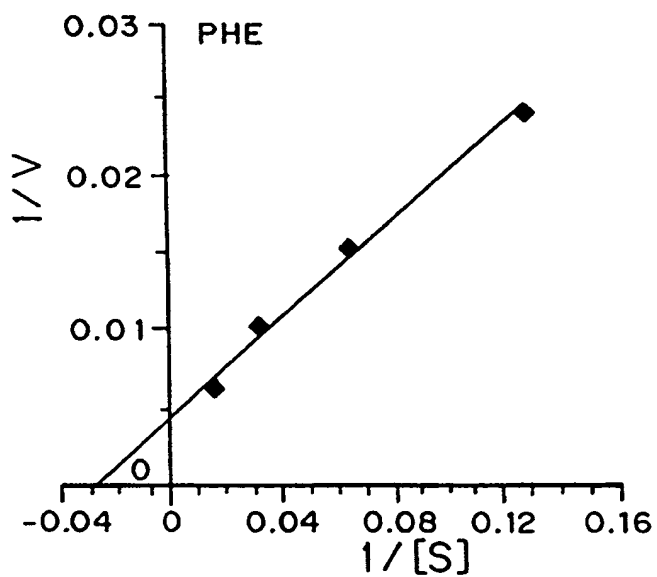
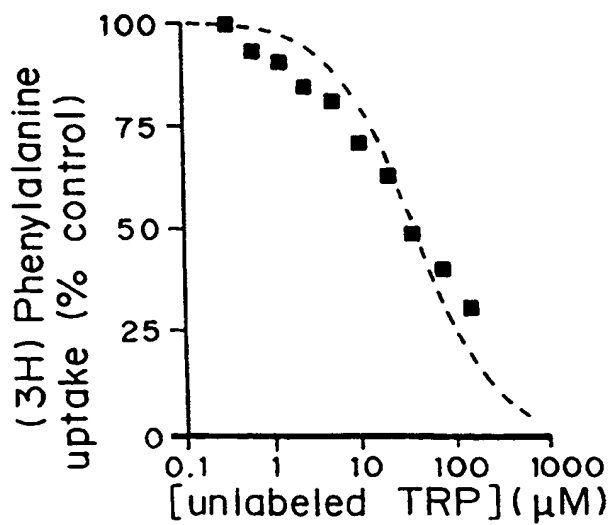
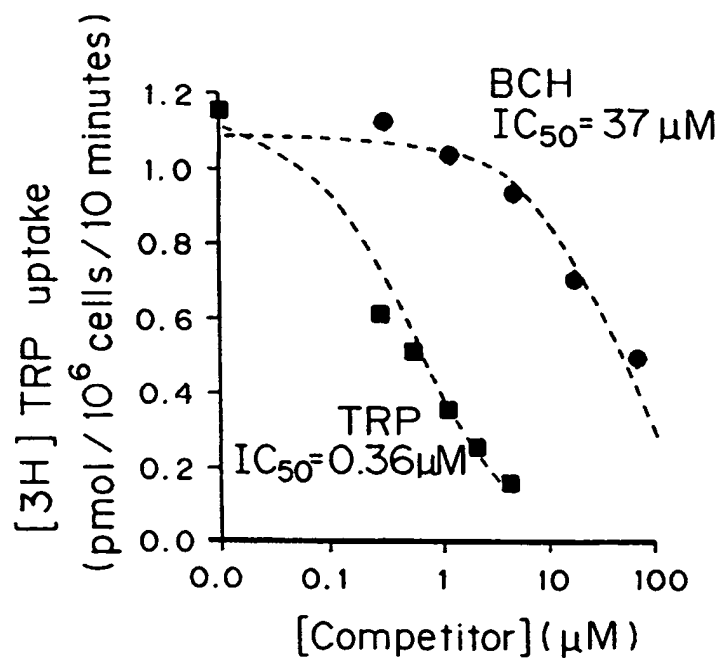
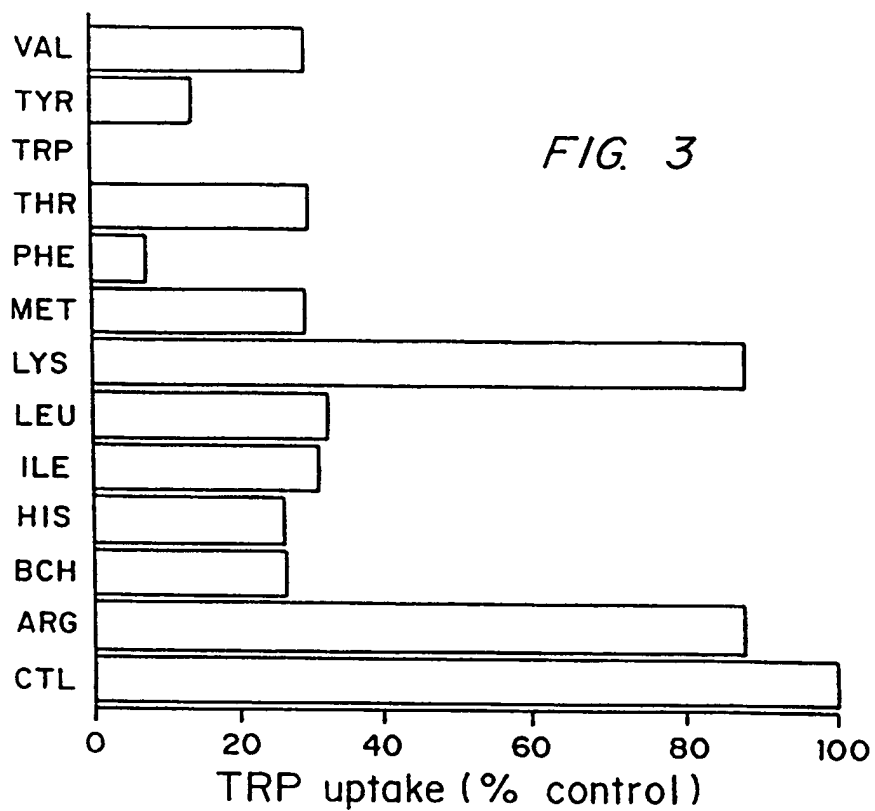


FIG. 2C





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*FIG. 4A*

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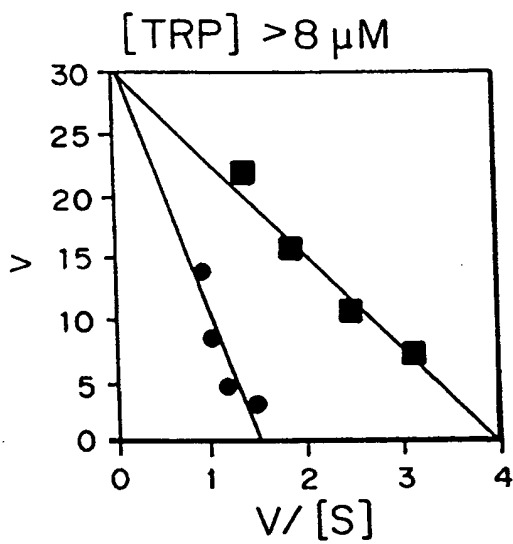


FIG. 4B

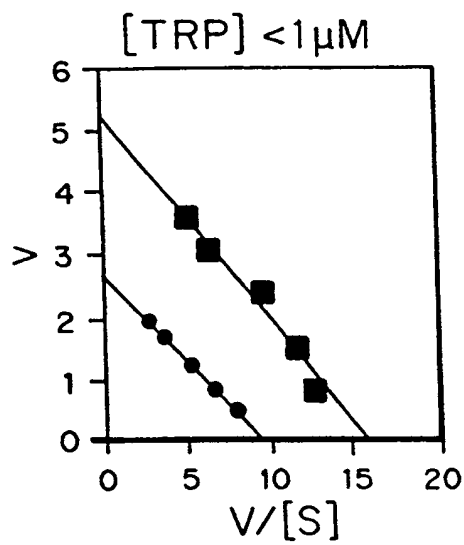


FIG. 4C

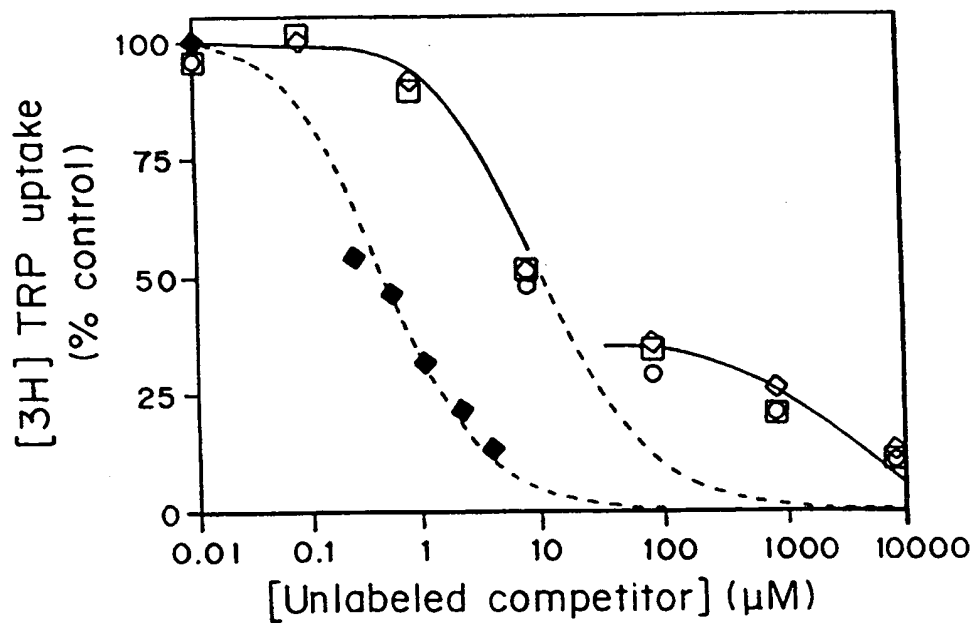


FIG. 5

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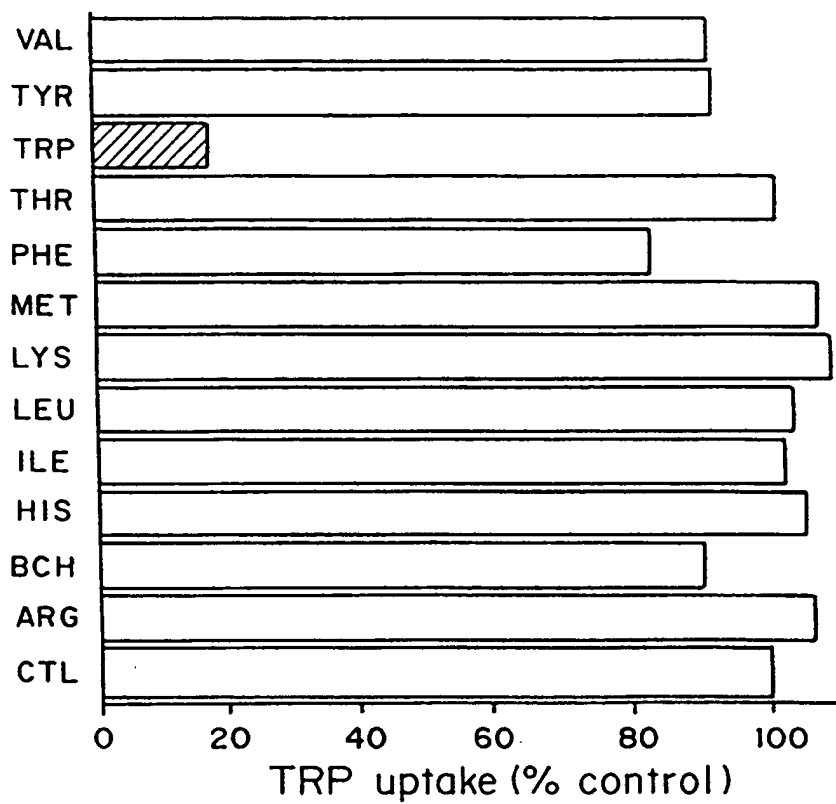


FIG. 6

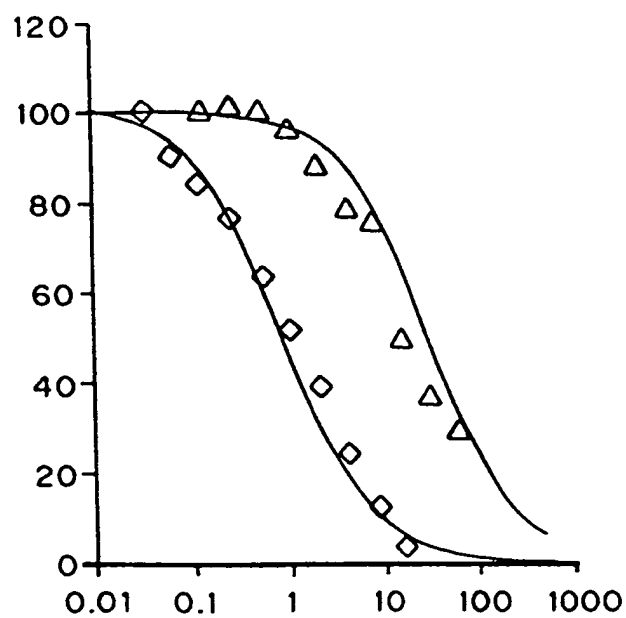


FIG. 7

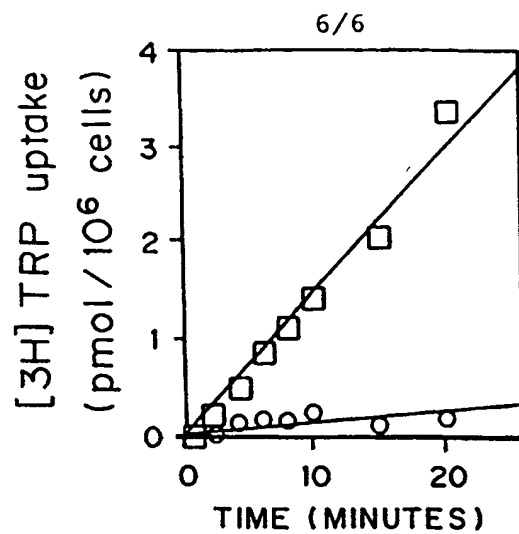


FIG. 8

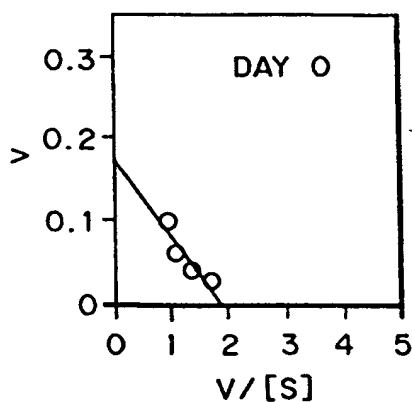


FIG. 9A

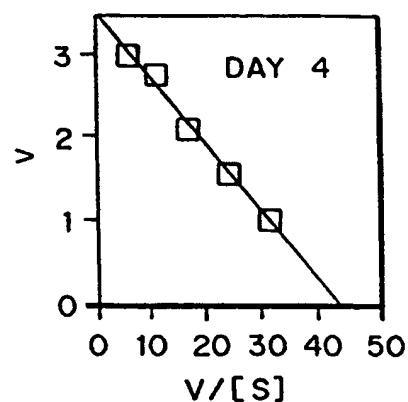


FIG. 9B

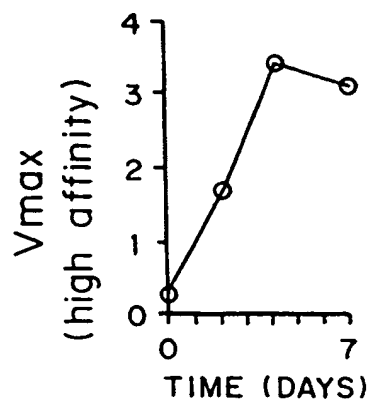


FIG. 9C

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/25841

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C07K14/47 A01K67/027

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	SEYMOUR R AND MUNN D H: "Identification and characterization of a novel, high-affinity tryptophan-selective transport system in human macrophages" BLOOD, vol. 90, no. 10, supplement 1(Part 1 of 2), 15 November 1997, page 448a XP002097470 See abstract 1987(46-IV) --- -/--	1

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Date of the actual completion of the international search

23 March 1999

Date of mailing of the international search report

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Cupido, M

# INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/25841

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ATTWOOD J T T: "The role of tryptophan depletion in T cell suppression by macrophages." IMMUNOLOGY, vol. 92, no. supplement 1, December 1997, page 7 XP002097471 See Abstract 2.7	1
O,X	& 5TH ANNUAL CONGRESS OF THE BRITISH SOCIETY FOR IMMUNOLOGY, 2-5 DECEMBER 1997 BRIGHTON, UK; PRESENTED ON TUESDAY, 2 DECEMBER, SESSION 2: TOLERANCE., -----	1

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